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ORIGINALLY FILES

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Huston, James S. Houston, L. L. Ring, David B. Oppermann, Hermann
- (ii) TITLE OF INVENTION: Biosynthetic Binding Proteins For Imaging
- (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS: (A) ADDRESSEE: Testa, Hurwitz & Thibeault/Patent Department
 - (B) STREET: Exchange Place, 53 State Street
 - (C) CITY: Boston
 - (D) STATE: Massachusetts
 - (E) COUNTRY: USA (F) ZIP: 02109
 - (V) COMPUTER READABLE FORM:
 - (A) HEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/HS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Kelley, Robin D.
 - (B) REGISTRATION NUMBER: 34,637
 - (C) REFERENCE/DOCKET NUMBER: 2054/22
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 617-248-7477
 - (B) TELEFAX: 617-248-7100
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 909 base pairs (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear



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(ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 3752 (D) OTHER INFORMATION: /product= "741F8 sFv' C-terminal Gly4-Cys"	MAR 2 8 2002 TECH CENTER 1600/2900
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:	2900
CC ATG GCG GAG ATC CAA TTG GTG CAG TCT GGA CCT GAG CTG AAG AAG Met Ala Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys 1 10 15	47
CCT GGA GAG ACA GTC AAG ATC TCC TGC AAG GCT TCT GGG TAT ACC TTC Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe 20 25 30	95
ACA AAC TAT GGA ATG AAC TGG GTG AAG CAG GCT CCA GGA AAG GGT TTA Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu 35 40 45	143
AAG TGG ATG GGC TGG ATA AAC ACC AAC ACT GGA GAG CCA ACA TAT GCT Lys Trp Het Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala 50 55 60	191
GAA GAG TTC AAG GGA CGG TTT GCC TTC TCT TTG GAA ACC TCT GCC AGC Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser 65 70 75	239
ACT GCC TAT TTG CAG ATC AAC AAC CTC AAA AAT GAG GAC ACG GCT ACA Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr 80 85 90 95	287
TAT TTC TGT GGA AGG CAA TTT ATT ACC TAC GGC GGG TTT GCT AAC TGG Tyr Phe Cys Gly Arg Gln Phe Ile Thr Tyr Gly Gly Phe Ala Asn Trp 100 105 110	335
GGC CAA GGG ACT CTG GTC ACT GTC TCT GCA TCG AGC TCC TCC GGA TCT Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ser Ser Ser Ser Gly Ser 115	383
TCA TCT AGC GGT TCC AGC TCG AGC GAT ATC GTC ATG ACC CAG TCT CCT Ser Ser Ser Gly Ser Ser Ser Ser Asp Ile Val Het Thr Gln Ser Pro 130 135 140	431
AAA TTC ATG TCC ACG TCA GTG GGA GAC AGG GTC AGC ATC TCC TGC AAG Lys Phe Het Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ser Cys Lys 145 150 155	479





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GCC Nla	AGT Ser	CAG Gln	GAT Asp	GTG Val	AGT Ser 165	ACT Thr	GCT Ala	GTA Val	GCC Ala	TGG Trp 170	TAT Tyr	CAA Gln	CAA Gln	AAA Lys	CCA Pro 175		527
GGG Gly	CAA Gln	TCT Ser	CCT Pro	AAA Lys 180	CTA Leu	CTG Leu	ATT Ile	TAC Tyr	TGG Trp 185	ACA Thr	TCC Ser	ACC Thr	CGG Arg	CAC His 190	ACT Thr		575
GGA Gly	GTC Val	CCT Pro	GAT Asp 195	CGC Arg	TTC Phe	ACA Thr	GGC Gly	AGT Ser 200	GGA Gly	TCT Ser	GGG Gly	ACA Thr	GAT Asp 205	TAT Tyr	ACT Thr		623
CTC Leu	ACC Thr	ATC Ile 210	Ser	AGT Ser	GTG Val	CAG Gln	GCT Ala 215	GAA Glu	GAC Asp	CTG Leu	GCA Ala	CTT Leu 220	ura	TAC Tyr	TGT Cys		671
CAG Gln	CAA Gln 225	CAT His	TAT Tyr	AGA Arg	GTG Val	CCG Pro 230	TAC Tyr	ACG Thr	TTC Phe	GGA Gly	GGG Gly 235	GLy	ACC Thr	AAG Lys	CTG Leu		719
GAG Glu 240	Ile	AAA Lys	CGG	GCT Ala	GAT Asp 245	GGG Gly	GGA Gly	GGT Gly	GGA Gly	TGT Cys 250		CGGG	GGA	GGTG	GATGTT		772
GGG	TCTC	GTT	ACGT	TGCG	GA T	CTCG	AGGC	TA T	CTTT	ACTA	ACT	CTTA	CCG	TAAA	GTTCTG	;	832
															TCGACC		892
	AGGC																909

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 250 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) HOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
- Met Ala Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro 1 5 10 15
- Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr 20 25 30
- Asn Tyr Gly Het Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys



Trp Het Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys Gly Arg Gln Phe Ile Thr Tyr Gly Gly Phe Ala Asn Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ser Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser Ser Ser Asp Ile Val Het Thr Gln Ser Pro Lys 135 Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ser Cys Lys Ala 150 Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu His Tyr Cys Gln 215 210 Gln His Tyr Arg Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Gly Gly Gly Cys

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 779 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA



(ix) FEATURE:

- (A) NAME/KEY: CDS (B) LOCATION: 3..758
- (D) OTHER INFORMATION: /product= "26-10 sFv' with C-terminal Gly4-Cys"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

	(* *)	360	ζΟ LLIV	ים טי	3000		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	, Du								_	
CC A	TG (let (GAA (Glu V	GTT (Val (CAA (Gln I	CTG (Leu (5	CAA (Gln (CAG T	CT C	GT (CCT (Pro (GAA T Glu I	TG (Leu \	GTT A	JAA (CT Pro 15		47
GGC Gly	GCC Ala	TCT Ser	GTG Val	CGC Arg 20	ATG Het	TCC Ser	TGC Cys	AAA Lys	TCC Ser 25	TCT Ser	GGG Gly	TAC Tyr	ATT Ile	TTC Phe 30	ACC Thr		95
GAC Asp	TTC Phe	TAC Tyr	ATG Met 35	AAT Asn	TGG Trp	GTT Val	CGC Arg	CAG Gln 40	TCT Ser	CAT His	GGT Gly	AAG Lys	TCT Ser 45	CTA Leu	GAC Asp		143
TAC Tyr	ATC Ile	GGG Gly 50	TAC Tyr	ATT Ile	TCC Ser	CCA Pro	TAC Tyr 55	TCT Ser	GGG Gly	GTT Val	ACC Thr	GGC Gly 60	TAC Tyr	AAC Asn	CAG Gln		191
AAG Lys	TTT Phe 65	AAA Lys	GGT Gly	AAG Lys	GCG Ala	ACC Thr 70	CTT Leu	ACT Thr	GTC Val	GAC Asp	AAA Lys 75	TCT Ser	TCC Ser	TCA Ser	ACT Thr		239
GCT Ala 80	TAC Tyr	ATG Met	GAG Glu	CTG Leu	CGT Arg 85	TCT Ser	TTG Leu	ACC Thr	TCT Ser	GAG Glu 90	GAC Asp	TCC Ser	GCG Ala	GTA Val	TAC Tyr 95		287
TAT Tyr	TGC Cys	GCG Ala	GGC Gly	TCC Ser 100	TCT Ser	GGT Gly	AAC Asn	AAA Lys	TGG Trp 105	GCC Ala	ATG Het	GAT Asp	TAT Tyr	TGG Trp 110	Gly		335
CAT His	GGT Gly	GCT Ala	AGC Ser 115	GTT Val	ACT Thr	GTG Val	AGC Ser	TCC Ser 120	TCC Ser	GGA Gly	TCT Ser	TCA Ser	TCT Ser 125	AGC Ser	GGT Gly		383
TCC Ser	AGC Ser	TCG Ser 130	AGT Ser	GGA Gly	TCC Ser	GAC Asp	GTC Val 135	GTA Val	ATG Het	ACC Thr	CAG Gln	ACT Thr 140	CCG Pro	CTG Leu	TCT Ser		431
CTG Leu	CCG Pro 145	GTT Val	TCT Ser	CTG Leu	GGT Gly	GAC Asp 150	CAG Gln	GCT Ala	TCT Ser	ATT Ile	TCT Ser 155	TGC Cys	CGC Arg	TCT Ser	TCC Ser		479
CAG Gln 160	TCT Ser	CTG Leu	GTC Val	CAT His	TCT Ser 165	Asn	GGT Gly	AAC Asn	ACT Thr	TAC Tyr 170	CTG Leu	AAC Asn	TGG Trp	TAC Tyr	CTG Leu 175		527



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									TEC	H CEI	VTER	1600	1/2900	٦		
CAA Gln	AAG Lys	GCT Ala	GGT Gly	CAG Gln 180	TCT Ser	CCG Pro	AAG Lys	CTT Leu	CTG	ATC	TAC	AAA	GTC	TCT	AAC Asn	575
CGC Arg	TTC Phe	TCT Ser	GGT Gly 195	GTC Val	CCG Pro	GAT Asp	CGT Arg	TTC Phe 200	TCT Ser	GGT Gly	TCT Ser	GGT Gly	TCT Ser 205	GGT Gly	ACT Thr	623
GAC Asp	TTC Phe	ACC Thr 210	CTG Leu	AAG Lys	ATC Ile	TCT Ser	CGT Arg 215	GTC Val	GAG Glu	GCC Ala	GAA Glu	GAC Asp 220	CTG Leu	GGT Gly	ATC	671
TAC Tyr	TTC Phe 225	TGC Cys	TCT Ser	CAG Gln	ACT Thr	ACT Thr 230	CAT His	GTA Val	CCG Pro	CCG Pro	ACT Thr 235	TTT Phe	GGT Gly	GGT Gly	GGC Gly	719
ACC Thr 240	AAG Lys	CTC Leu	GAG Glu	ATT Ile	AAA Lys 245	CGT Arg	TCC Ser	GGG Gly	GGA Gly	GGT Gly 250	GGA Gly	TGT Cys	TAAC	CTGC	\GC	768
CCG	GGG4	ATC (779
(2)	INFO	ORMA!	rion	FOR	SEQ	ID 1	10:4	:								
	((i) :	(A) (B)	LEN TYI	GTH:		2 am:			5						
		` '	(A) (B) (D)	LEN TYI TOI	GTH: PE: 6	: 252 emino	2 am: o ac: Line:	ino a id ar		5						
	(:	ii) l	(A) (B) (D)	LEN TYN TON	GTH: PE: 6 POLOG	: 252 emino GY: 1 E: p1	2 am: o ac: linea	ino a id ar in	acid	NO:	4:					
Het 1	(:	ii) ki)	(A) (B) (D) HOLEC	LENCE	GTH: PE: 4 POLOG TYPI DESG	: 252 emino GY: 1 E: pr	2 am: o ac: line: rote:	ino a id ar in : SE	acid:	₩0:		Val	Lys	Pro 15	бlу	
1	(: (:	ii) l ki) : Val	(A) (B) (D) fiOLEC SEQUI	LEN TYI TOI CULE ENCE Leu	GTH: PE: 2 POLOG TYPI DESG	: 252 amino GY: 1 E: pr CRIP:	2 am: o ac: Linea rote: rION	ino a id ar in : SEG	Q ID Pro 10	NO:	Leu			15		
1 Ala	(i (i Glu	ii) l ki) : Val	(A) (B) (D) folio SEQUI Gln Arg 20	LENCE Leu 5	GTH: CE: 6 COLOG TYPE DESC Gln Ser	E: process of the control of the con	2 am: b ac: linearote: rION Ser	ino a id ar in SEG Gly Ser 25	Q ID Pro 10 Ser	NO:	Leu Tyr	Ile	Phe 30	15 Thr	Asp	
Ala Phe	(i Glu Ser	ii) l ki) : Val Val Het 35	(A) (B) (D) fiOLE(SEQUI Gln Arg 20 Asn	LENCE Leu S Ket	GTH: PE: 2 POLOG TYPI DESG Gln Ser Val	E: 252 E: pr CRIPT Gln Cys Arg	2 am: 5 ac: 6 ac: 1 ine: 1 TON Ser Lys Gln 40	ino a id ar in Gly Ser 25	Q ID Pro 10 Ser His	NO: Glu Gly Gly	Leu Tyr Lys	Ile Ser 45	Phe 30 Leu	Thr Asp	Asp Tyr	
Ala Phe	(i Glu Ser Tyr	ii) val Val Het 35	(A) (B) (D) (IOLEO GIN Arg 20 Asn	LEN TYN TOI CULE Leu S Het	Pro	: 252 mmino GY: 1 CRIPT Gln Cys Arg Tyr 55 Leu	2 am b acclined rote: FION Ser Lys Gln 40	ino idinar in SEG Gly Ser 25 Ser	Q ID Pro 10 Ser His	NO: Glu Gly Gly Thr	Leu Tyr Lys Gly 60	Ile Ser 45	Phe 30 Leu Asn	Thr Asp Gln	Asp Tyr Lys	



Cys Ala Gly Ser Ser Gly Asn Lys Trp Ala Het Asp Tyr Trp Gly His

Gly Ala Ser Val Thr Val Ser Ser Ser Gly Ser Ser Ser Gly Ser

Ser Ser Ser Gly Ser Asp Val Val Het Thr Gln Thr Pro Leu Ser Leu

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln 150

Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu Gln

Lys Ala Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg 180

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr

Phe Cys Ser Gln Thr Thr His Val Pro Pro Thr Phe Gly Gly Gly Thr 230 225

Lys Leu Glu Ile Lys Arg Ser Gly Gly Gly Gly Cys

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 739 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..729
- (D) OTHER INFORMATION: /product= "520C9 sFv polypeptide sequence"

	(xi)	SEQ	UENC	E DE	SCRI	PTIC	N: S	EQ I	D N O	:5:							
GAG Glu 1	ATC Ile	CAA Gln	TTG Leu	GTG Val 5	CAG Gln	TCT Ser	GGA Gly	CCT Pro	GAG Glu 10	CTG Leu	AAG Lys	AAG Lys	CCT Pro	GGA Gly 15	GAG Glu	48	
ACA Thr	GTC Val	AAG Lys	ATC Ile 20	TCC Ser	TGC Cys	AAG Lys	GCT Ala	TCT Ser 25	GGA Gly	TAT Tyr	ACC Thr	TTC Phe	GCA Ala 30	AAC Asn	TAT Tyr	96	
GGA Gly	ATG Met	AAC Asn 35	TGG Trp	ATG Het	AAG Lys	CAG Gln	GCT Ala 40	CCA Pro	GGA Gly	AAG Lys	GGT Gly	TTA Leu 45	AAG Lys	TGG Trp	ATG Het	144	
GGC Gly	TGG Trp 50	ATA Ile	AAC Asn	ACC Thr	TAC Tyr	ACT Thr 55	GGA Gly	CAG Gln	TCA Ser	ACA Thr	TAT Tyr 60	GCT Ala	GAT Asp	GAC Asp	TTC Phe	192	
AAG Lys 65	GAA Glu	CGG Arg	TTT Phe	GCC Ala	TTC Phe 70	TCT Ser	TTG Leu	GAA Glu	ACC Thr	TCT Ser 75	GCC Ala	ACC Thr	ACT Thr	GCC Ala	CAT His 80	240	1
TTG Leu	CAG Gln	ATC Ile	AAC Asn	AAC Asn 85	CTC Leu	AGA Arg	AAT Asn	GAG Glu	GAC Asp 90	TCG Ser	GCC Ala	ACA Thr	TAT Tyr	TTC Phe 95	TGT Cys	288	1
GCA Ala	AGA Arg	CGA Arg	TTT Phe 100	GGG Gly	TTT Phe	GCT Ala	TAC Tyr	TGG Trp 105	GLY	CAA Gln	GGG Gly	ACT Thr	CTG Leu 110	GTC Val	AGT Ser	336	•
GTC Val	TCT Ser	GCA Ala 115	Ser	ATA Ile	TCG Ser	AGC Ser	TCC Ser 120	Ser	GGA Gly	TCT Ser	TCA Ser	TCT Ser 125	AGC Ser	GGT Gly	TCC Ser	384	•
AGC Ser	TCG Ser 130	Ser	GGA Gly	TCC Ser	GAT Asp	ATC Ile 135	Gln	ATG	ACC	CAG Gln	TCT Ser 140	Pro	TCC Ser	TCC Ser	TTA Leu	432	2
TCT Ser 145	Ala	TCT Ser	CTG Leu	GGA Gly	GAA Glu 150	Arg	GTC Val	AGT Ser	CTC Leu	ACT Thr 155	Cys	CGG Arg	GCA Ala	AGT Ser	CAG Gln 160	480	Э
GAC Asp	ATT	GGT	AAT Asn	AGC Ser 165	Leu	ACC	TGC	CTI Let	CAC Glr 170	i Gin	GAA Glu	CCA Pro	GAT Asp	GGA Gly 175	ACT Thr	52	8
ATT Ile	: Lys	Arg	; Leu	Ile	TAC Tyr	Ala	1 Thi	: Sei	r Sei	TTA Leu	GAT L Asp	TCI Ser	GGT Gly 190	101	CCC Pro	57	6



AAA Lys	AGG Arg	TTC Phe 195	AGT Ser	GGC Gly	AGT Ser	CGG Arg	TCT Ser 200	GGG Gly	TCA Ser	GAT Asp	TAT Tyr	TCT Ser 205	CTC Leu	ACC Thr	ATC Ile
AGT Ser	AGC Ser 210	CTT Leu	GAG Glu	TCT Ser	GAA Glu	GAT Asp 215	TTT Phe	GTA Val	GTC Val	TAT Tyr	TAC Tyr 220	TGT Cys	CTA Leu	CAA Gln	TAT Tyr
GCT Ala 225	ATT Ile	TTT Phe	CCG Pro	TAC Tyr	ACG Thr 230	TTC Phe	GGA Gly	GGG Gly	GGG Gly	ACC Thr 235	AAC Asn	CTG Leu	GAA Glu	ATA Ile	AAA Lys 240
	GCT Ala	GAT Asp	TAAT	rctg(CAG										
(2)	INFO	RHAT	поп	FOR	SEQ	ID N	₹0:6:	:							
	((i) S	(A) (B)	LEI TYI	GTH:	243 uming		ino a id	: acids	5					
	(:	ii) h	OLE	CULE	TYP	: p1	otei	in							
	,														
	()	(1)	SEQUI	ENCE	DESC	CRIP	CION:	: SE) ID	NO:	5:				
Glu 1									Glu 10			Lys	Pro	Gly 15	Glu
1	Ile	Gln	Leu	Val 5	Gln	Ser	Gly	Pro	Glu	Leu	Lys			15	
1 Thr	Ile Val	Gln Lys	Leu Ile 20	Val 5 Ser	Gln Cys	Ser Lys	Gly Ala	Pro Ser 25	Glu 10	Leu Tyr	Lys Thr	Phe	Ala 30	15 Asn	Tyr
1 Thr Gly	Ile Val Het	Gln Lys Asn 35	Leu Ile 20 Trp	Val 5 Ser Met	Gln Cys Lys	Ser Lys Gln	Gly Ala Ala 40	Pro Ser 25 Pro	Glu 10 Gly	Leu Tyr Lys	Lys Thr Gly	Phe Leu 45	Ala 30 Lys	Asn Trp	Tyr Ket
Thr Gly Gly	Ile Val Het Trp 50	Gln Lys Asn 35 Ile	Leu Ile 20 Trp Asn	Val 5 Ser Met	Gln Cys Lys Tyr	Ser Lys Gln Thr 55	Gly Ala Ala 40 Gly	Pro Ser 25 Pro Gln	Glu 10 Gly Gly	Leu Tyr Lys Thr	Lys Thr Gly Tyr 60	Phe Leu 45 Ala	Ala 30 Lys Asp	Asn Trp Asp	Tyr Het Phe
Thr Gly Gly Lys 65	Val Het Trp 50	Gln Lys Asn 35 Ile Arg	Leu Ile 20 Trp Asn Phe	Val 5 Ser Met Thr	Gln Cys Lys Tyr Phe 70	Lys Gln Thr 55 Ser	Gly Ala Ala 40 Gly Leu	Pro Ser 25 Pro Gln Glu	Glu 10 Gly Gly Ser	Leu Tyr Lys Thr Ser 75	Lys Thr Gly Tyr 60 Ala	Phe Leu 45 Ala Thr	Ala 30 Lys Asp	Asn Trp Asp	Tyr Het Phe His
Thr Gly Gly Lys 65 Leu	Ile Val Met Trp 50 Glu Gln	Gln Lys Asn 35 Ile Arg	Leu Ile 20 Trp Asn Phe	Val 5 Ser Met Thr Ala Asn 85 Gly	Gln Cys Lys Tyr Phe 70 Leu	Ser Lys Gln Thr 55 Ser	Gly Ala Ala 40 Gly Leu Asn	Pro Ser 25 Pro Gln Glu Glu	Glu 10 Gly Gly Ser Thr Aspp 90	Leu Tyr Lys Thr Ser 75	Lys Thr Gly Tyr 60 Ala	Phe Leu 45 Ala Thr	Ala 30 Lys Asp Thr	Asn Trp Asp Ala Phe 95 Val	Tyr Het Phe His 80 Cys



Ser Ser Ser Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu 130 135 140

Ser Ala Ser Leu Gly Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln 145 150 155 160

Asp Ile Gly Asn Ser Leu Thr Trp Leu Gln Glu Pro Asp Gly Thr 165 170 175

Ile Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro 180 185 190

Lys Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile

Ser Ser Leu Glu Ser Glu Asp Phe Val Val Tyr Tyr Cys Leu Gln Tyr 210 215 220

Ala Ile Phe Pro Tyr Thr Phe Gly Gly Gly Thr Asn Leu Glu Ile Lys 225 230 240

Arg Ala Asp

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..15
 - (D) OTHER INFORMATION: /note= "Linker 1"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser 15



- (2) INFORMATION FOR SEQ ID NO:8:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..15
 - (D) OTHER INFORMATION: /note= "LINKER 2"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Ser Ser Gly Ser Ser Ser Gly Ser Ser Ser Gly

- (2) INFORMATION FOR SEQ ID NO:9:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein

 - (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..2
 - (D) OTHER INFORMATION: /note= "C-Terminal Tail (Ser-Cys)"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ser Cys

1

- (2) INFORMATION FOR SEQ ID NO:10:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /note= "C-Terminal Tail (Gly-Gly-Gly-Cys)"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Gly Gly Gly Cys

- (2) INFORMATION FOR SEQ ID NO:11:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE: (A) NAME/KEY: Protein
 - (B) LOCATION: 1..11

 - (D) OTHER INFORMATION: /note= "C-Terminal Tail (His-His-His-His-His-Gly-Gly-Gly-Cys) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

His His His His His Gly Gly Gly Cys